SEQUENCE LISTING

<110> Consortium fuer elektrochemische Industrie [Consortium for electrochemical industry] GmbH

<120> Cells and method for fermentatively preparing R-α-lipoic acid

<130> Co10314

<140>
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<160> 4

<170> PatentIn Ver. 2.0

<210> 1
<211> 679
<212> DNA
<213> Escherichia coli

<220>
<221> CDS
<222> (16)..(654)
<223> lipB gene

<300>
<301> Reed, Kelynne E.
Cronan Jr., John E.
<302> Lipoic Acid Metabolism in Escherichia coli: Sequencing and Functional Characterization of the lipA and lipB Genes
<303> J. Bacteriol.
<304> 175
<305> 5
<306> 1325-1336
<307> 1993

<400> 1

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cacggagatg cccat atg tat cag gat aaa att ctt gtc cgc cag ctc ggt  51
                Met Tyr Gln Asp Lys Ile Leu Val Arg Gln Leu Gly
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ctt cag cct tac gag cca atc tcc cag gct atg cat gaa ttc acc gat  99
Leu Gln Pro Tyr Glu Pro Ile Ser Gln Ala Met His Glu Phe Thr Asp
        15                  20                  25

acc cgc gat gat agt acc ctt gat gaa atc tgg ctg gtc gag cac tat 147
Thr Arg Asp Asp Ser Thr Leu Asp Glu Ile Trp Leu Val Glu His Tyr
    30                  35                  40

ccg gta ttc acc caa ggt cag gca gga aaa gcg gag cac att tta atg 195
Pro Val Phe Thr Gln Gly Gln Ala Gly Lys Ala Glu His Ile Leu Met
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ccg ggt gat att ccg gtg atc cag agc gat cgc ggt ggg cag gtg act   243
Pro Gly Asp Ile Pro Val Ile Gln Ser Asp Arg Gly Gly Gln Val Thr
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tat cac ggg ccg ggg caa cag gtg atg tat gtg ttg ctt aac ctg aaa   291
Tyr His Gly Pro Gly Gln Gln Val Met Tyr Val Leu Leu Asn Leu Lys
            80                  85                  90

cgc cgt aaa ctc ggt gtg cgt gaa ctg gtg acc ttg ctt gag caa aca   339
Arg Arg Lys Leu Gly Val Arg Glu Leu Val Thr Leu Leu Glu Gln Thr
        95                  100                 105

gtg gtg aat acc ctg gct gaa ctg ggt ata gaa gcg cat cct cgg gct   387
Val Val Asn Thr Leu Ala Glu Leu Gly Ile Glu Ala His Pro Arg Ala
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gac gcg cca ggt gtc tat gtt ggg gaa aag aaa att tgc tca ctg ggt   435
Asp Ala Pro Gly Val Tyr Val Gly Glu Lys Lys Ile Cys Ser Leu Gly
125                 130                 135                 140

tta cgt att cga cgc ggt tgt tca ttc cac ggt ctg gca tta aac gtc   483
Leu Arg Ile Arg Arg Gly Cys Ser Phe His Gly Leu Ala Leu Asn Val
                145                 150                 155

aat atg gat ctt tca cca ttt tta cgt att aat cct tgt ggg tat gcc   531
Asn Met Asp Leu Ser Pro Phe Leu Arg Ile Asn Pro Cys Gly Tyr Ala
            160                 165                 170

gga atg gaa atg gct aaa ata tca caa tgg aaa ccc gaa gcg acg act   579
Gly Met Glu Met Ala Lys Ile Ser Gln Trp Lys Pro Glu Ala Thr Thr
        175                 180                 185

aat aat att gct cca cgt tta ctg gaa aat att tta gcg cta cta aac   627
Asn Asn Ile Ala Pro Arg Leu Leu Glu Asn Ile Leu Ala Leu Leu Asn
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aat ccg gac ttc gaa tat att acc gct taattccata catcaatggc ccaat   679
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Ser Thr Leu Asp Glu Ile Trp Leu Val Glu His Tyr Pro Val Phe Thr
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Gln Gly Gln Ala Gly Lys Ala Glu His Ile Leu Met Pro Gly Asp Ile
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Pro Val Ile Gln Ser Asp Arg Gly Gly Gln Val Thr Tyr His Gly Pro
 65                  70                  75                  80

Gly Gln Gln Val Met Tyr Val Leu Leu Asn Leu Lys Arg Arg Lys Leu
                85                  90                  95

Gly Val Arg Glu Leu Val Thr Leu Leu Glu Gln Thr Val Val Asn Thr
            100                 105                 110

Leu Ala Glu Leu Gly Ile Glu Ala His Pro Arg Ala Asp Ala Pro Gly
        115                 120                 125

Val Tyr Val Gly Glu Lys Lys Ile Cys Ser Leu Gly Leu Arg Ile Arg
    130                 135                 140

Arg Gly Cys Ser Phe His Gly Leu Ala Leu Asn Val Asn Met Asp Leu
145                 150                 155                 160

Ser Pro Phe Leu Arg Ile Asn Pro Cys Gly Tyr Ala Gly Met Glu Met
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Ala Lys Ile Ser Gln Trp Lys Pro Glu Ala Thr Thr Asn Asn Ile Ala
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<222> (1)..(258)
<223> E2 domain hybrid gene

<300>
<301> Miles, John S.
Guest, John R.
<302> Subgenes expressing single lipoyl domains of the dehydrogenase complex of Escherichia coli
<303> Biochem. J.
<304> 245
<306> 869-874
<307> 1987

<300>
<301> Ali, Sohail T.
Guest, John R.
<302> Isolation and characterisation of lipoylated and unlipoylated domains of the E2p subunit of the pyruvate dehydrogenase complex of Echerichia coli
<303> Biochem. J.
<304> 271
<306> 139-145
<307> 1990

<400> 3

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atg gct atc gaa atc aaa gta ccg gac atc ggg gct gat gaa gtt gaa   48
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atc acc gag atc ctg gtc aaa gtg ggc gac aaa gtt gaa gcc gaa cag   96
Ile Thr Glu Ile Leu Val Lys Val Gly Asp Lys Val Glu Ala Glu Gln
             20                  25                  30

tcg ctg atc acc gta gaa ggc gac aaa gct tct atg gaa gtt ccg gcg  144
Ser Leu Ile Thr Val Glu Gly Asp Lys Ala Ser Met Glu Val Pro Ala
         35                  40                  45

ccg ttt gca ggc gtc gtg aag gaa ctg aaa gtc aac gtt ggc gat aaa  192
Pro Phe Ala Gly Val Val Lys Glu Leu Lys Val Asn Val Gly Asp Lys
     50                  55                  60

gtg aaa act ggc tcg ctg att atg atc ttc gaa gtt gaa ggc gca gcg  240
Val Lys Thr Gly Ser Leu Ile Met Ile Phe Glu Val Glu Gly Ala Ala
 65                  70                  75                  80

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Ser Leu Ile Thr Val Glu Gly Asp Lys Ala Ser Met Glu Val Pro Ala
         35                  40                  45

Pro Phe Ala Gly Val Val Lys Glu Leu Lys Val Asn Val Gly Asp Lys
     50                  55                  60
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Val Lys Thr Gly Ser Leu Ile Met Ile Phe Glu Val Glu Gly Ala Ala
 65                  70                  75                  80

Pro Ala Ala Ala Pro Ala
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<220>
<221> CDS
<222> (1)..(261)
<223> BCCP-DASMEP domain gene

<300>
<301> Reche, Pedro
Perham, Richard N.
<302> Structure and selectivity in post-translational modification: attaching the biotinyl-lysine and lipoyl-lysine swinging arms in multifunctional enzymes.
<303> EMBO J.
<304> 18
<305> 10
<306> 2673-2682
<307> 1999

<400> 5

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atg gaa gcg cca gca gca gcg gaa atc agt ggt cac atc gta cgt tcc   48
Met Glu Ala Pro Ala Ala Ala Glu Ile Ser Gly His Ile Val Arg Ser
  1               5                  10                  15

ccg atg gtt ggt act ttc tac cgc acc cca agc ccg gac gca aaa gct   96
Pro Met Val Gly Thr Phe Tyr Arg Thr Pro Ser Pro Asp Ala Lys Ala
            20                  25                  30

ttc atc gaa gtg ggt cag aaa gtc aac gtg ggc gat acc cta tgc atc   144
Phe Ile Glu Val Gly Gln Lys Val Asn Val Gly Asp Thr Leu Cys Ile
        35                  40                  45

gtt gaa gcc gac aaa gca tcg atg gaa atc ccg gcg gac aaa tcc ggt   192
Val Glu Ala Asp Lys Ala Ser Met Glu Ile Pro Ala Asp Lys Ser Gly
    50                  55                  60

acc gtg aaa gca att ctg gtc gaa agt gga caa ccg gta gaa ttt gac   240
Thr Val Lys Ala Ile Leu Val Glu Ser Gly Gln Pro Val Glu Phe Asp
65                  70                  75                  80

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Glu Pro Leu Val Val Ile Glu
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            20                  25                  30

Phe Ile Glu Val Gly Gln Lys Val Asn Val Gly Asp Thr Leu Cys Ile
        35                  40                  45

Val Glu Ala Asp Lys Ala Ser Met Glu Ile Pro Ala Asp Lys Ser Gly
    50                  55                  60

Thr Val Lys Ala Ile Leu Val Glu Ser Gly Gln Pro Val Glu Phe Asp
65                  70                  75                  80

Glu Pro Leu Val Val Ile Glu
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